



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/050,898

DATE: 01/27/2003 TIME: 09:46:25

Input Set : A:\1700.0190005seqlist.txt
Putput Set: N:\CRF4\01242003\J050898.raw

```
7 :: 110 - APPLICANT: Renner, Wolfgang A.
                       Bachmann, Martin
                       Tissot, Alain
1::
                      Maorer, Patrick
11
                      Lechner, Franziska
1.
                      Selkel, Peter
1:
                      Piessek, Christine
1.4
                      Orthann, Earner
15.
                      Lucka, Fainer
16,
                      Staurenhiel, Matthias
17
                       Frey, Peter
19 <120> TITLE OF INVENTION: Molecular Antigen Array
21 -: 130 > FILE REFERENCE: 1700.0190005
.3 ×140 × CUPPENT APPLICATION NUMBER: 10/050,898
.4 -:141 - CUFRENT FILING DATE: 2002-01-18
16 -: 150 - PEIGE APPLICATION NUMBER: US 60/262,379
.7 -: 151 - PRIOR F!LIDA DATE: 1001-01-19
29 -150 - PETOE APPLICATION NUMBER: US 60/288,549
70 -1101 - PRIOS FILING DATE: 7001-05-04
 FI -: 150 - PRIOF APPLICATION NUMBER: US 60/326,998
33 -: 1:1: PRION FILING DATE: 7001-10-05
35 150 - PEIOF APPLICATION NUMBER: US 60/331,045
36 H151 - PRIOR FILING DATE: 1001-11-07
38 H160 NUMBER OF SEQ ID NOS: 350
40 - 170 > SOFTWARE: Patentin Ver. 2.1
42 K210 / SEQ II NO: 1
45 -0011 - LENGTH: 41
44 KOID'S TYFE: DNA
45 - 1213 * OFGAMISM: Artificial Sequence
47 KILO - FEATURE:
49 -000 ar OTHER INFORMATION: Primer
January Regulation: 1
10 ugguacgogt qoaqsaqqta accaccgtta aagaaggcac c
                                                                                                                                                                                     41
54 HINDS SEQ ID NO: 3
!! Hall - LENGTH: 44
16 -UNIO TYPE: DNA
17 MITTO OFGANISM: Artificial Sequence
La FILLE FEATURE:
60 HUNES OTHER INFORMATION: Primer
60 H4000 SECUENCE: 2
to oggraphic objects of control of the control of t
                                                                                                                                                                                    44
(6 THOUSE, ID NO: 3
```

67 < 211: LENGTH: 20

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68 -C212> TYPE: DUA 69 KM C ORGANIAM: Astificial Sequence VI H. DEL FEATUPE: 71 C.L. CTHEE INFORMATION: Primer 74 HARRY SEQUENCE: 3 20 75 ocatgagges targatacco 78 -0.100 SEQ 11: NO: 4 79 -0011: IEDGTH: .5 80 HILL TYPE: DIW 81 -0.130 OFGAULEM: Astificial Sequence 83 -0.00 FEATUFF: 84 HOLDS OTHER INFORMATION: Primer 86 KI400 - SEQUENCE: 4 25 87 ggdantsand godidestta dagge 90 HO160 SEQ II NO: 5 91 - C11 - LENGTH: 47 95 KILL TYPE: DNA 93 -001% OFGANISM: Artificial Sequence 95 ROSCON FEATURE: 96 KINBS OTHER INFORMATION: Primer 98 <400> SEQUENCE: 5 99 cettetttaa euguggttac etgetggeaa ecaaegtggt teatgac 47 102 - 2100 SEQ IS NO: 6 103 /011: LENGTH: 40 104 - DIA TYPE: DNA 105 - 113 - OEGANISM: Artificial Sequence 107 KING FEATURE: 108 KDAR OTHER INFORMATION: Primer 110 <400. SEQUENCE: € 40 111 algoalanty capacityty oggtyglogg alogocoggo 114 - 210 - SEQ ID NO: 7 115 K211 | LENGTH: 90 116 KULD - TYPE: DNA 117 <213 - OFGANISM: Artificial Sequence 119 -0000 - FEATURE: 120 -0.13 - OTHER INFORMATION: Primer 112 <400 · SEQUENCE: 7 1/3 gggtotagat trocaaceat tecettated aggettittg acaaegetat geteegegee 60 174 catogratiqui accagatggo attigadado 117 -010 - SEQ ID NO: 8 11s . 11 - DEMOTH: 11s 1. A + . B. + TYPE: DUA 1:0 -0013 - OEGANIOM: Artificial Sequence 1 TO SELECT FEATURE: 133 AUG 3 - OTHER INFORMATION: Primer 1% + 400 + SEQUEDCE: 8170 grythtagwa qyaggtaaaa aacgatgaaa wagacagota togogattgo agtggcactg 60

13/ aptautting stadogtage graggootte scaaccatte cettated

140 (210 / SEQ ID NO: 9

108

PATENT APPLICATION: US/10/050,898

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Input Set : A:\1700.0190005seqlist.txt
Output Set: N:\CRF4\01242003\J050898.raw

141 · 011 LEWSTH: 01	
142 + 11 TYPE: DNA	
143 - 13 - OF WANTEM: Artificial Sequence	
145 + 220 + FEATUFF:	
140 · OTHER INFORMATION: Primer	
148 + 400 + EFRUENCE: 9	
149 gangaarting tagaagecae agetgeeete e	31
152 0210 03EQ 110 NO: 10	
104 . 111 . 1810999	
154 - LTJ - FYFE: DNA	
155 - 113 - OFGANICM: Artificial Sequence	
157 - 100 - FEATUFE:	
15% - LT: - OTHER INFORMATION: Primer	
160 × 400 × CEQUENCE: 10	
161 catacadata tot recegae acce	24
164 - 110 - MEQ II NO: 11	
165 - 111 LEDGIH: 41	
166 - /11 - TYFE: DIA	
167 - 717 - OFCANISM: Artificial Sequence	
169 - HRO - FEATURE:	
170 <023 OTHER INFORMATION: Primer	
170 - 400 - SEQUEDOE: 11	
17: cowegaaga googoaa boaccgtgtg begecaggat g	41
176 - 30 - 3F0 Th No: 12	
177 + 211 + LEUGTH: 37	
178 - 112 - TYPE: DNA	
179 F.C. D. CANTON: Artifletial Sequence	
181 - 0.00 - FEATURE:	
18. FILT OTHER INFORMATION: Primer	
184 - 400 - SEQUEDOE: 02	
185 stateateta gaatgaatag aggattettt aac	33
188 K210 + SEQ IF NO: 13	
189 ×3115 LENGTH: 15	
190 KO125 TYFE: DNA	
191 k013% OFGANISM: Artificial Sequence	
193 × 200 × FRATURE:	
194 · .: 3 · OTHER INFORMATION: Modified ribosome binding site	
197 + 400	
198 aggagtasa saadg	15
- 000 - 10 - 350 IP NO: 14	
0.0 + 0.1 + 0.6 MgTh: 0.1	
1.03 s.712 TYPE: PRT	
1004 - 113 - OFGANISM: Artificial Sequence	
1006 - 100 - FEATURE:	
207 - 233 OTHER INFORMATION: signal peptide	
210 - 400 - SEQUENCE: 14	
211 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala	
212 1 5 10 15	
214 Frr Val Ala 31n Ala	
21 1,12 101 1100 D1 1 1000	

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!nput Set : A:\1700.0190005seqlist.txt
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```
215
118 - 105 SED IE 10: 15
1.19 - .11 % LENGTH: 46
130 + 21 + TYLE: PF1
...1 - ... - GEGANI:NA: Artificial Sequence
:23 - ... G - FEATUFE:
.33 - ... - OTHER INFORMATION: modified Fos construct
her - 460 - Pequence: 15
128 Cys Gly Gly Lea Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu
                                           1:)
. 29 1
                       5
INT Asp. Glo Lys Ser Ala Led Gln Thr Glu Ile Ala Asn Led Led Lys Glu
                                      2.5
                 234 Lys Glo Lys Let Glu Phe Ile Leu Ala Ala His Gly Gly Cys
                                   40
             ÷ €,
79% - 210 - 2EQ II: No: 16
_39 + 11 + LENGTH: →
240 - 12 - TYLE: PHT
141 - 213 - OFGANISM: Artificial Sequence
243 / 200 FEATURE:
244 - 223 - OTHER INFORMATION: peptide linker
146 -400 - PEQUENCE: 16
247 Ala Ala Ala Ser Gly Gly
. 4%
353 ×210 × SEQ ID 30: 17
255 ×211 × LENGTH: €
159 - 110 - TYFB: PRT
354 - 213 - 0FGANISM: Artificial Sequence
156 - JOON FEATURE:
157 - 221 - OTHER INFORMATION: Description of Artificial Sequence: pertide linker
259 <4000 SEQUEDCE: 17
,60 Gly Gly Ser Ala Ala Ala
161 1
264 <210% SEQ ID NO: 18
 065 2011 - LENGTH: 256
166 FILES TYPE: DNA
167 × 213 · OPGAMISM: Artificial Sequence
269 kDUON FEATURE:
170 KURRY OTHER INFORMATION: Fos fusion construct
.73 - 4000 MEQUENCE: 18
173 minitonipa mg. siwaaad gatgamaaag ahagotatog ogattgbagt ggoadtggot 60
.74 pg:troppha horrageda ggeotgogtg ggggeggeeg elletggtgg tigeggtggt 120
275 etgaecquea ecetydaggo ggaaacegad caggtggaag acgaaaaato ogogotgcaa 180
176 anomalating ogalahotgot gaaagaaaaa gaaaagstgg agttoatoot ggoggoacac 240
                                256
. 77 maragettact badant
(∂) -210 - SBQ H NO: 19
US1 - U11 - DENGTH: 50
. 82 - LII - TYPE: FFT
.83 ... 3 · O. SAMISM: Artificial Sequence
 LB5 - P20 - FEATURE:
```

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DATE: 01/27/2003

Input Set : A:\1700.0190005seqlist.txt
Output Set: N:\CRF4\01242003\J050898.raw

```
186 < 225 CTHER INFOFMATION: Fos fusion construct
1-3 <400 SEQUENCE: 19
189 Al. Ala Ala Ser Guy Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
                                           10
1901 O.: Thr Amp Gin Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
                                                           .30
                                      25
                . `(:
.90 Alu Ash Lou Leo Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
                                  40
296 55
29% His Gly Gly Cys
599 50
30% -110 - SEQ II NO: 20
404 + 211 + BENGTH: ..61
ROG + MIN - TYPE: DNA
NUM - 11:0 ORGANISM: Artificial Sequence
208 - MOO - FEATURE:
MOW - 1. 4 - OTHER INFORMATION: For fusion construct
FILE OF FEATURE:
312 - L1 - MAME/KEY: CDS
11: - PICE - LOCATION: (22)..(240)
315 -400 - SEQUENCE: 20
\pm 1.6 unaltoagga qqtaasmaac q atq aaa aag aca got ato gog att goa g{
m tg}
                             Met Lys Lys Thr Ala Ile Ala Ile Ala Val
111
318
_{
m EO}0 geW ofg got ggt the get abougta gog dag god tge ggt ggt etg acc
                                                                          99
3.1 Ala Leu Ala Gly Phe Ala Thr Val Ala Glm Ala Cys Gly Gly Leu Thr
                                           .: 0
                      1.5
\pm 0.4 dam acc ctg dag dog gaa acc gad dag gtg gaa gad gaa aaa too gog
                                                                          147
5.75 Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala
                                       35
                 <u>-</u>.1)
 30.6
 32% ong cas acc gas ato gog aac otg ong asa gas aas gas aag oog gag
                                                                          195
 379 bou Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu
                                   50
             45
 332 the ato etg geg gea cae ggt ggt tgc ggt ggt tet geg gee get
                                                                          240
 333 Pho Ile Deu Ala Ala His Gly Gly Cys Gly Sly Ser Ala Ala Ala
                                                    70
                               65
         6.0
 334
                                                                          261
 336 gggtgtgggg atatcaaget t
 339 -1100 SEC ID NO: 21
 340 - 2115 LENGTH: 73
 341 - Ji. :- TYPE: FFT
 -- . . . OR WANIEM: Astificial Sequence
 944 - THE FEATURES
 :45 - . Par OTHER INFORMATION: For fusion construct
 :42 - 4:0 - SEQUENCE: 01
 344 Met bys bys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
                                           10
 NO. 1
 19. Thr Val Ala Gun Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu
                                       5.5
                                                            3.0
                  20
 355 Thr Asp Glr Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala
                                   4.0
 356
```

RAW SEQUENCE LISTING ERROR SUMMARY PATENT APPLICATION: US/10/050,898

DATE: 01/27/2003 TIME: 09:46:26

Input Set : A:\1700.0190005seqlist.txt
Output Set: N:\CRF4\01242003\J050898.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:111; Xaa Pos. 28
Seq#:283; N Pos. 9820

VERIFICATION SUMMARY

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Input Set : A:\1700.0190005seqlist.txt
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L:2389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:111 after pos.:16

L:5193 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (177) SEQUENCE:

L:9617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:283 after pos.:9780